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PCT

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/719,485

DATE: 07/05/2001

TIME: 15:43:06

Input Set : A:\20251p.txt

Output Set: N:\CRF3\07032001\I719485.raw

ENTERED

4 <110> APPLICANT: Feighner, Scott D.
5 Patchett, Arthur A.
6 Tan, Carina
7 McKee, Karen Kulju
8 MacNeil, Douglas
9 Howard, Andrew D.
10 Pong, Sheng-Shung
11 Smith, Roy G.
13 <120> TITLE OF INVENTION: CLONING AND IDENTIFICATION OF THE
14 MOTILIN RECEPTOR
16 <130> FILE REFERENCE: 20251P
18 <140> CURRENT APPLICATION NUMBER: 09/719,485
C--> 19 <141> CURRENT FILING DATE: 2001-05-25
21 <150> PRIOR APPLICATION NUMBER: PCT/US99/12773
22 <151> PRIOR FILING DATE: 1999-06-08
24 <150> PRIOR APPLICATION NUMBER: 60/089,098
25 <151> PRIOR FILING DATE: 1998-06-12
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29 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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32 <211> LENGTH: 3066
33 <212> TYPE: DNA
34 <213> ORGANISM: Homo sapiens
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39 cgaaaccctg actacacaaa aaacacaaaa tttagccggg gcttgggcgc tcctgtgctc	180
40 ccagctactc aggaggctga ggtgggagga ctgcttgagc ctgggaggtc gaggctgcag	240
41 tgagctgtga tcgcgccact taaactccag cctggacgac agtgagacc tgtctcaaga	300
42 agaaaaaag aaagaaagaa agaaaaaag aaaaaaaga aattatttgg tcaattatat	360
43 ggtcagctcc ctccaccact cgcgaattta cagaagagga gaactgggct gggcgagacc	420
44 aggactagcc caagattaca caagttactc ggttgtagag ccaggattag acaggagagg	480
45 ctctagattc tgggtctagac tcccctccta ttatttagca ttatggcttc ctgaggatta	540
46 ccatgagccc tctctcaccg tcaagcggca gctaccagcc accagaccag atcccttcga	600
47 aggtgcccgg agtaccagac tgacaaaagc gcccgtagag tgctcagtc tgtaaccaa	660
48 gctgtctagg gtgcagacat cgctcaccgg accgggtagg gctcgtgcgc taagggcgc	720
49 gggattacca gttagtggag aggggaagcgc cctggaactg catgggcccg ggagagggcg	780
50 cgggagcgga gcatggccgg gccggggcg gccggggccg tgggaggaga ctgcgcgcag	840
51 ctagctcggg agcgcctcgg agcccacccc gcagagccgc ttctcgcgc ccgcagcgca	900
52 gcgcagcgct ccgcgctctg acctgccgcg ccgcgagcgt gcgggctggg aaaggaggcg	960
53 ctacccgaga gggaccacgc gccaggctcc cagcccagcc cgggacgcgg cgcccgcgcg	1020
54 gagcacccat gggcagcccc tggaaacggca gcgacggccc cgagggggcg cgggagccgc	1080
55 cgtggcccg gctgcgcctg tgcgacgagc gccgctgctc gccctttccc ctgggggcgc	1140
56 tgggtccggg gaccgctgtg tgctgtgccc tggctcgtc cggggtgagc ggcaacgtgg	1200
57 tgagcgtgat gctgatcggg cgctaccggg acatgcggac caccaccaac ttgtacctgg	1260
58 gcagcatggc cgtgtccgac ctactcatcc tgcctgggct gccgttcgac ctgtaccgcc	1320
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60 gcgagggctg cacctacgcc acgctgctgc acatgaccgc gctcagcgtc gagcgtacc 1440
61 tggccatctg ccgcccgcgc cgcgcgcgcg tcttggtcac ccggcgccgc gtccgcgcgc 1500
62 tcatcgctgt gctctgggccc gtggcgctgc tctctgccgg tcccttcttg ttcctgggtg 1560
63 gcgtcgagca ggaccccggc atctcogtag tcccgggcct caatggcacc gcgcggatcg 1620
64 cctcctcgcc tctgcctcg tgcgcgcctc tctggctctc gcgggcgcca ccgcgcctcc 1680
65 cgccgtcggg gcccgagacc gcggaggccg cggcgctggt cagccgcgaa tgccggccga 1740
66 gcccgcgcga gctgggcgcg ctgctgttca tgcgtggtt caccaccgcc tacttcttcc 1800
67 tgccctttct gtgcctcagc atcctctacg ggctcatcgg gcgggagctg tggagcagcc 1860
68 ggcgccgcgt gcgaggcccg gccgcctcgg ggccggagag aggccaccgg cagaccgtcc 1920
69 gcgtcctgcg taagtggagc cgcctggtt ccaaagacgc ctgcctgcag tccgcccgcg 1980
70 cggggaccgc gcaaacgctg ggtccccttc cctgctcgc ccagctctgg gcgcgccttc 2040
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73 cggatccgat tcagtaacca gcagtgttt tccagagcct ctgagaccag aaaggagagt 2220
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82 aatcccgggt ctgtgtctta tgttcagtg gtggtggttc tggcatttat aatttgcctg 2760
83 ttgcccttcc acgttggcag aatcatttac ataaacacgg aagattcgcg gatgatgtac 2820
84 ttctctcagt actttaacat cgtcgtctg caacttttct atctgagcgc atctatcaac 2880
85 ccaatcctct acaacctcat ttcaaagaag tacagagcgg cggcctttta actgctgtc 2940
86 gcaaggaggt ccaggccgag aggtctccac agaagcaggg aactgcggg ggaagttgca 3000
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98 gtgaccgctg tgtgcctgtg cctgttccgc gtcggggtga gcggcaacgt ggtgaccgtg 180
99 atgctgatcg ggcgctaccg ggacatgcgg accaccacca acttgtacct gggcagcatg 240
100 gcctgttcgc acctactcat cctgctcggg ctgcgcgttc acctgtaccg cctctggcgc 300
101 tgcgcggcct ggggtgttcgg gccgctgtc tgcgcctgt cctctacgt gggcgagggc 360
102 tgcaacctac ccacgctgct gcacatgacc gcgtcagcg tcgagcgcta cctggccatc 420
103 tgccgcgcgc tcgcgcgcgc cgtcttggtc acccggcgc gcgtccgcgc gctcatcgtc 480
104 gtgctctggg ccgtggcgct gctctctgcc ggtcccttct tgttccgtgt gggcgtcgag 540
105 caggaccccg gcactcctgt agtcccgggc ctcaatggca ccgcgcggat cgcctcctcg 600
106 cctctgcctc cgtgcgcgc tctctggctc tgcggggcgc caccgcgcgc cccgcgcgtc 660
107 gggcccgaga ccgcggaggc cgcggcgctg ttcagccgcg aatgccggcc gagccccgcg 720
108 cagctgggcg cgtgcgtgt catgctgtgg gtcaccacc cctacttctt cctgcccctt 780
109 ctgtgcctca gcactcctta cgggctcctc gggcgggagc tgtggagcag ccggcgccgc 840
110 ctgcgaggcc cggcgcgcctc gggcggggag agaggccacc ggcagaccgt ccgcgtcctg 900

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111 ctggtggtgg ttctggcatt tataatttgc tgggttgcct tccacgttgg cagaatcatt      960
112 tacataaaca cggaagattc gcggatgatg tactttctctc agtactttaa catcgtcgct      1020
113 ctgcaacttt tctatctgag cgcatctatc aacccaatcc tctacaacct catttcaaag      1080
114 aagtacagag cggcggcctt taaactgctg ctgcgaagga agtccaggcc gagaggcttc      1140
115 cacagaagca gggacactgc gggggaagtt gcaggggaca ctggaggaga cacggtgggc      1200
116 tacaccgaga caagcgctaa cgtgaagacg atgggataa      1239
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120 <212> TYPE: PRT
121 <213> ORGANISM: Homo sapiens
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126 Pro Pro Trp Pro Ala Leu Pro Pro Cys Asp Glu Arg Arg Cys Ser Pro
127 20 25 30
128 Phe Pro Leu Gly Ala Leu Val Pro Val Thr Ala Val Cys Leu Cys Leu
129 35 40 45
130 Phe Val Val Gly Val Ser Gly Asn Val Val Thr Val Met Leu Ile Gly
131 50 55 60
132 Arg Tyr Arg Asp Met Arg Thr Thr Thr Asn Leu Tyr Leu Gly Ser Met
133 65 70 75 80
134 Ala Val Ser Asp Leu Leu Ile Leu Leu Gly Leu Pro Phe Asp Leu Tyr
135 85 90 95
136 Arg Leu Trp Arg Ser Arg Pro Trp Val Phe Gly Pro Leu Leu Cys Arg
137 100 105 110
138 Leu Ser Leu Tyr Val Gly Glu Gly Cys Thr Tyr Ala Thr Leu Leu His
139 115 120 125
140 Met Thr Ala Leu Ser Val Glu Arg Tyr Leu Ala Ile Cys Arg Pro Leu
141 130 135 140
142 Arg Ala Arg Val Leu Val Thr Arg Arg Arg Val Arg Ala Leu Ile Ala
143 145 150 155 160
144 Val Leu Trp Ala Val Ala Leu Leu Ser Ala Gly Pro Phe Leu Phe Leu
145 165 170 175
146 Val Gly Val Glu Gln Asp Pro Gly Ile Ser Val Val Pro Gly Leu Asn
147 180 185 190
148 Gly Thr Ala Arg Ile Ala Ser Ser Pro Leu Ala Ser Ser Pro Pro Leu
149 195 200 205
150 Trp Leu Ser Arg Ala Pro Pro Pro Ser Pro Pro Ser Gly Pro Glu Thr
151 210 215 220
152 Ala Glu Ala Ala Ala Leu Phe Ser Arg Glu Cys Arg Pro Ser Pro Ala
153 225 230 235 240
154 Gln Leu Gly Ala Leu Arg Val Met Leu Trp Val Thr Thr Ala Tyr Phe
155 245 250 255
156 Phe Leu Pro Phe Leu Cys Leu Ser Ile Leu Tyr Gly Leu Ile Gly Arg
157 260 265 270
158 Glu Leu Trp Ser Ser Arg Arg Pro Leu Arg Gly Pro Ala Ala Ser Gly
159 275 280 285
160 Arg Glu Arg Gly His Arg Gln Thr Val Arg Val Leu Leu Val Val Val
161 290 295 300

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162 Leu Ala Phe Ile Ile Cys Trp Leu Pro Phe His Val Gly Arg Ile Ile
163 305                      310                      315                      320
164 Tyr Ile Asn Thr Glu Asp Ser Arg Met Met Tyr Phe Ser Gln Tyr Phe
165                      325                      330                      335
166 Asn Ile Val Ala Leu Gln Leu Phe Tyr Leu Ser Ala Ser Ile Asn Pro
167                      340                      345                      350
168 Ile Leu Tyr Asn Leu Ile Ser Lys Lys Tyr Arg Ala Ala Ala Phe Lys
169                      355                      360                      365
170 Leu Leu Leu Ala Arg Lys Ser Arg Pro Arg Gly Phe His Arg Ser Arg
171                      370                      375                      380
172 Asp Thr Ala Gly Glu Val Ala Gly Asp Thr Gly Gly Asp Thr Val Gly
173 385                      390                      395                      400
174 Tyr Thr Glu Thr Ser Ala Asn Val Lys Thr Met Gly
175                      405                      410

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177 <210> SEQ ID NO: 4

178 <211> LENGTH: 1390

179 <212> TYPE: DNA

180 <213> ORGANISM: Homo sapiens

182 <400> SEQUENCE: 4

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185 gtgaccgctg tgtgcctgtg cctgttcgtc gtgggggtga gcggcaacgt ggtgaccgtg      180
186 atgctgatcg ggcgtaccg ggacatgcgg accaccacca acttgtaact gggcagcatg      240
187 gccgtgtccg acctactcat cctgctcggg ctgcccgttcg acctgtaccg cctctggcgc      300
188 tcgcgccctt ggtgttcgg gccgctgctc tgcccgtgtt cctctactcg gggcgagggc      360
189 tgcacctacg ccacgctgct gcacatgacc gcgctcagcg tcgagcgcta cctggccatc      420
190 tgccgcccgc tccgcgcccg cgtcttggtc acccggcgcg gcgtccgcgc gctcatcgct      480
191 gtgctctggg ccgtggcgct gctctctgcc ggtcccttct tgttccctgt gggcgtcgag      540
192 caggaccccg gcatctccgt agtcccgggc ctcaatggca ccgcgcggat cgcctcctcg      600
193 cctctcgcct cgctcgccgc tctctggctc tcgcgggcgc caccgcccgc cccgcccgtc      660
194 gggcccagag ccgcggaggg cgcggcgctg ttcagccgcg aatgccggcc gagcccgcg      720
195 cagctggggc cgtgcgtgt catgctgtgg gtcaccaccg cctacttctt cctgcccttt      780
196 ctgtgcctca gcatcctcta cgggtcctac gggcgggagc tgtggagcag ccggcgcccg      840
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199 gcgcaaacgc tgggtcccct tcccgtgctc gccagctct gggcgccgct tccagctccc      1020
200 ttctctatct cgattccagc ctccaccgcg cgtggtggtg gttctggcat ttataatttg      1080
201 ctggttgccc ttccacgttg gcagaatcat ttacataaac acggaagatt cgcggatgat      1140
202 gtactttctt cagtacttta acatcgctgc tctgcaactt ttctatctga gcgcatctat      1200
203 caacccaatc ctctacaacc tcatttcaaa gaagtacaga gcggcgccct ttaactgct      1260
204 gctcgcaagg aagtccaggc cgagaggctt ccacagaagc agggacactg cgggggaagt      1320
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209 <211> LENGTH: 386

210 <212> TYPE: PRT

211 <213> ORGANISM: Homo sapiens

213 <400> SEQUENCE: 5

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215 1 5 10 15
216 Pro Pro Trp Pro Ala Leu Pro Pro Cys Asp Glu Arg Arg Cys Ser Pro
217 20 25 30
218 Phe Pro Leu Gly Ala Leu Val Pro Val Thr Ala Val Cys Leu Cys Leu
219 35 40 45
220 Phe Val Val Gly Val Ser Gly Asn Val Val Thr Val Met Leu Ile Gly
221 50 55 60
222 Arg Tyr Arg Asp Met Arg Thr Thr Thr Asn Leu Tyr Leu Gly Ser Met
223 65 70 75 80
224 Ala Val Ser Asp Leu Leu Ile Leu Leu Gly Leu Pro Phe Asp Leu Tyr
225 85 90 95
226 Arg Leu Trp Arg Ser Arg Pro Trp Val Phe Gly Pro Leu Leu Cys Arg
227 100 105 110
228 Leu Ser Leu Tyr Val Gly Glu Gly Cys Thr Tyr Ala Thr Leu Leu His
229 115 120 125
230 Met Thr Ala Leu Ser Val Glu Arg Tyr Leu Ala Ile Cys Arg Pro Leu
231 130 135 140
232 Arg Ala Arg Val Leu Val Thr Arg Arg Arg Val Arg Ala Leu Ile Ala
233 145 150 155 160
234 Val Leu Trp Ala Val Ala Leu Leu Ser Ala Gly Pro Phe Leu Phe Leu
235 165 170 175
236 Val Gly Val Glu Gln Asp Pro Gly Ile Ser Val Val Pro Gly Leu Asn
237 180 185 190
238 Gly Thr Ala Arg Ile Ala Ser Ser Pro Leu Ala Ser Ser Pro Pro Leu
239 195 200 205
240 Trp Leu Ser Arg Ala Pro Pro Pro Ser Pro Pro Ser Gly Pro Glu Thr
241 210 215 220
242 Ala Glu Ala Ala Ala Leu Phe Ser Arg Glu Cys Arg Pro Ser Pro Ala
243 225 230 235 240
244 Gln Leu Gly Ala Leu Arg Val Met Leu Trp Val Thr Thr Ala Tyr Phe
245 245 250 255
246 Phe Leu Pro Phe Leu Cys Leu Ser Ile Leu Tyr Gly Leu Ile Gly Arg
247 260 265 270
248 Glu Leu Trp Ser Ser Arg Arg Pro Leu Arg Gly Pro Ala Ala Ser Gly
249 275 280 285
250 Arg Glu Arg Gly His Arg Gln Thr Val Arg Val Leu Arg Lys Trp Ser
251 290 295 300
252 Arg Arg Gly Ser Lys Asp Ala Cys Leu Gln Ser Ala Pro Pro Gly Thr
253 305 310 315 320
254 Ala Gln Thr Leu Gly Pro Leu Pro Leu Leu Ala Gln Leu Trp Ala Pro
255 325 330 335
256 Leu Pro Ala Pro Phe Pro Ile Ser Ile Pro Ala Ser Thr Arg Arg Gly
257 340 345 350
258 Gly Gly Ser Gly Ile Tyr Asn Leu Leu Val Ala Leu Pro Arg Trp Gln
259 355 360 365
260 Asn His Leu His Lys His Gly Arg Phe Ala Asp Asp Val Leu Leu Ser
261 370 375 380
262 Val Leu
263 385

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VERIFICATION SUMMARY

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L:19 M:271 C: Current Filing Date differs, Replaced Current Filing Date